

GenCore version 5.1.3  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: February 27, 2003, 06:39:18 ; Search time 86 Seconds

(without alignments)

4691.643 Million cell updates/sec

Title: US-09-677-653A-50

Sequence: 1 MGDAGVASGRPHNRGTRNV.....GKIARVRRARRARRARAN 647

Scoring table:

BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 460893 segs, 311809382 residues

Total number of hits satisfying chosen parameters: 921786

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+.p2n.model -DEV=xlh  
-Q=/cgn2\_1/USPTO.spool/US09677653/rnat.20022003.164317.1369/app\_query.fasta.1.839  
-DB=Published.Applications.NA -QFMT=fastap -SUFFIX=p2n.rnpb -MINMATCH=0.1  
-LOOPEI=0 -LOOPEI=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62  
-TRANS=human40.cdi -LIST=45 -DOCALL=200 -THR SCORE=pct -THR MAX=100  
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0  
-MAXLEN=200000000 -USER=US09677653 -CGN\_1.1\_35\_etrnat.20022003.164317.1369  
-NCPU=6 -ICPU=3 -NO\_XLPXY -NO\_MMAR -LARGEQUERY -NEG\_SCORES=0 -WAIT -LONGLOG  
-DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published.Applications.NA:\*

1: /cgn2\_6/ptodata/1/pubpna/US07\_PUBCOMB.seq:\*  
2: /cgn2\_6/ptodata/1/pubpna/PCT\_NEW\_PUB.seq:\*  
3: /cgn2\_6/ptodata/1/pubpna/US06\_NEW\_PUB.seq:\*  
4: /cgn2\_6/ptodata/1/pubpna/US06\_PUBCOMB.seq:\*  
5: /cgn2\_6/ptodata/1/pubpna/US07\_NEW\_PUB.seq:\*  
6: /cgn2\_6/ptodata/1/pubpna/PCTUS\_PUBCOMB.seq:\*  
7: /cgn2\_6/ptodata/1/pubpna/US08\_NEW\_PUB.seq:\*  
8: /cgn2\_6/ptodata/1/pubpna/US08\_PUBCOMB.seq:\*  
9: /cgn2\_6/ptodata/1/pubpna/US09\_NEW\_PUB.seq:\*  
10: /cgn2\_6/ptodata/1/pubpna/US09\_PUBCOMB.seq:\*  
11: /cgn2\_6/ptodata/1/pubpna/US10\_NEW\_PUB.seq:\*  
12: /cgn2\_6/ptodata/1/pubpna/US10\_PUBCOMB.seq:\*  
13: /cgn2\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq:\*  
14: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match length	ID	Description
1	139.5	4.1	19031	US-09-070-927A-167
2	129	3.8	11739	US-09-070-927A-150
3	125.5	3.7	2748	US-09-821-616-33
4	124.5	3.7	7035	US-09-815-242-8615

5	117.5	3.5	81940	9	US-09-759-508B-1	Sequence 1, Appl1
6	117	3.5	2872	9 <td>US-10-025-380-1055</td> <td>Sequence 1055, Ap</td>	US-10-025-380-1055	Sequence 1055, Ap
7	117	3.5	2872	10 <td>US-09-922-217-1055</td> <td>Sequence 1055, Ap</td>	US-09-922-217-1055	Sequence 1055, Ap
8	117	3.5	2872	10 <td>US-09-833-263-1055</td> <td>Sequence 1055, Ap</td>	US-09-833-263-1055	Sequence 1055, Ap
9	116.5	3.5	1929	9 <td>US-09-554-000-1</td> <td>Sequence 1, Appl1</td>	US-09-554-000-1	Sequence 1, Appl1
10	116.5	3.5	1929	9 <td>US-09-554-000-5</td> <td>Sequence 5, Appl1</td>	US-09-554-000-5	Sequence 5, Appl1
11	116.5	3.5	1959	9 <td>US-09-554-000-3</td> <td>Sequence 3, Appl1</td>	US-09-554-000-3	Sequence 3, Appl1
12	116.5	3.5	1971	9 <td>US-09-554-000-7</td> <td>Sequence 7, Appl1</td>	US-09-554-000-7	Sequence 7, Appl1
13	116.5	3.5	3112	10 <td>US-09-917-800A-1543</td> <td>Sequence 1543, Ap</td>	US-09-917-800A-1543	Sequence 1543, Ap
14	116	3.4	5072	12 <td>US-10-044-090-640</td> <td>Sequence 640, Ap</td>	US-10-044-090-640	Sequence 640, Ap
15	113.5	3.4	25165	9 <td>US-10-114-170-39</td> <td>Sequence 39, Appl</td>	US-10-114-170-39	Sequence 39, Appl
16	113	3.3	2906	9 <td>US-10-114-170-186</td> <td>Sequence 186, Ap</td>	US-10-114-170-186	Sequence 186, Ap
17	112.5	3.3	1509	9 <td>US-09-738-626-2545</td> <td>Sequence 2545, Ap</td>	US-09-738-626-2545	Sequence 2545, Ap
18	111.5	3.3	1708	10 <td>US-09-822-830A-612</td> <td>Sequence 612, Ap</td>	US-09-822-830A-612	Sequence 612, Ap
19	111	3.3	4190	10 <td>US-09-962-832-1111</td> <td>Sequence 111, Ap</td>	US-09-962-832-1111	Sequence 111, Ap
20	110.5	3.3	3903	10 <td>US-09-815-242-3848</td> <td>Sequence 3848, Ap</td>	US-09-815-242-3848	Sequence 3848, Ap
21	110.5	3.3	3903	10 <td>US-09-815-242-6809</td> <td>Sequence 6809, Ap</td>	US-09-815-242-6809	Sequence 6809, Ap
22	110.5	3.3	4260	10 <td>US-09-925-302-196</td> <td>Sequence 196, Ap</td>	US-09-925-302-196	Sequence 196, Ap
23	110.5	3.3	4645	9 <td>US-09-971-536-27</td> <td>Sequence 27, Appl</td>	US-09-971-536-27	Sequence 27, Appl
24	109	3.2	3591	9 <td>US-10-098-841-45</td> <td>Sequence 45, Appl</td>	US-10-098-841-45	Sequence 45, Appl
25	109	3.2	3663	9 <td>US-10-098-841-44</td> <td>Sequence 44, Appl</td>	US-10-098-841-44	Sequence 44, Appl
26	109	3.2	3309400	9 <td>US-09-738-626-1</td> <td>Sequence 1, Appl1</td>	US-09-738-626-1	Sequence 1, Appl1
27	106.5	3.2	32768	10 <td>US-09-070-927A-399</td> <td>Sequence 399, Ap</td>	US-09-070-927A-399	Sequence 399, Ap
28	106	3.1	3914	12 <td>US-10-044-090-148</td> <td>Sequence 148, Ap</td>	US-10-044-090-148	Sequence 148, Ap
29	105.5	3.1	4530	9 <td>US-09-738-626-207</td> <td>Sequence 207, Ap</td>	US-09-738-626-207	Sequence 207, Ap
30	105.5	3.1	8772	10 <td>US-09-788-711A-3</td> <td>Sequence 3, Appl1</td>	US-09-788-711A-3	Sequence 3, Appl1
31	105.5	3.1	8771	10 <td>US-09-788-711A-1</td> <td>Sequence 1, Appl1</td>	US-09-788-711A-1	Sequence 1, Appl1
32	105.5	3.1	3309400	9 <td>US-09-738-626-1</td> <td>Sequence 1, Appl1</td>	US-09-738-626-1	Sequence 1, Appl1
33	105	3.1	2448	10 <td>US-09-860-846-36</td> <td>Sequence 4051, Ap</td>	US-09-860-846-36	Sequence 4051, Ap
34	105	3.1	4041	9 <td>US-09-860-846-36</td> <td>Sequence 36, Appl</td>	US-09-860-846-36	Sequence 36, Appl
35	105	3.1	4041	10 <td>US-09-861-289-36</td> <td>Sequence 5, Appl1</td>	US-09-861-289-36	Sequence 5, Appl1
36	105	3.1	36778	9 <td>US-09-860-846-5</td> <td>Sequence 5, Appl1</td>	US-09-860-846-5	Sequence 5, Appl1
37	105	3.1	36778	10 <td>US-09-861-289-5</td> <td>Sequence 5, Appl1</td>	US-09-861-289-5	Sequence 5, Appl1
38	104	3.1	7560	12 <td>US-10-100-912-3</td> <td>Sequence 3, Appl1</td>	US-10-100-912-3	Sequence 3, Appl1
39	104	3.1	7746	10 <td>US-09-778-927A-20</td> <td>Sequence 20, Appl</td>	US-09-778-927A-20	Sequence 20, Appl
40	104	3.1	13029	10 <td>US-09-815-242-4052</td> <td>Sequence 4052, Ap</td>	US-09-815-242-4052	Sequence 4052, Ap
41	103.5	3.1	2757	9 <td>US-09-788-626-3470</td> <td>Sequence 3470, Ap</td>	US-09-788-626-3470	Sequence 3470, Ap
42	103.5	3.1	88421	9 <td>US-09-976-059-1</td> <td>Sequence 1, Appl1</td>	US-09-976-059-1	Sequence 1, Appl1
43	103	3.1	1984	9 <td>US-10-146-474-5</td> <td>Sequence 5, Appl1</td>	US-10-146-474-5	Sequence 5, Appl1
44	103	3.1	2076	9 <td>US-09-938-842A-1260</td> <td>Sequence 1260, Ap</td>	US-09-938-842A-1260	Sequence 1260, Ap
45	102	3.0	1965	10 <td>US-09-826-660-26</td> <td>Sequence 26, Appl</td>	US-09-826-660-26	Sequence 26, Appl

#### ALIGNMENTS

RESULT 1  
US-09-070-927A-167  
; Sequence 167, Application US/09070927A  
; Patent No. US20020120116A1  
GENERAL INFORMATION:  
APPLICANT: Charles A. Kunsch  
Patrick J. Dillon  
Steven Barash  
TITLE OF INVENTION: Enterococcus faecialis Polynucleotides and Polypeptides  
NUMBER OF SEQUENCES: 982  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Human Genome Sciences, Inc.  
STREET: 9410 Key West Avenue  
CITY: Rockville  
STATE: Maryland  
COUNTRY: USA  
ZIP: 20850  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage  
COMPUTER: HP Vectra 486/33  
OPERATING SYSTEM: MSDOS version 6.2  
SOFTWARE: ASCII Text  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/070.927A  
FILING DATE: 04-May-2000  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/046.655



```

QY 476 SerPheGlyAlaValSerPhe-----AsnAsnProGlyThrGluArgThr 490
      :|:|:|:|:|:|
Db 5902 AAAAAAGTTCAAGTCTTCAACACTCCGCAACAGGAAACCAACACTGTTTGA 5961
QY 491 ArgAspLeuProAspTyrThrGlyIleArgAspSerPheAspIleAsnMetSerThrAla 510
      :|:|:|:|:|:|
Db 5962 GCAGAGTTGTAGTATGTGTATTAAGATAGTACAGTGCATTAACCTTC----- 6012
QY 511 ValAlaHisPheArgSerLeuSerHisSerCysSerIleValThrIleThrIleGly 530
      :|:|:|:|:|:|
Db 6013 -----GTGAGATTCTGTCCAATGTATCAAGAGTGTACACACACAGCAGGAGGC 6063
QY 531 TTPGluGlyValThrAsnValAsnThrProPheGlyGluPheAlaHisIleGlyLeuLeu 550
      :|:|:|:|:|:|
Db 6064 TTCATCAGTGTGCACACCTTCGAC-----TTCGGCCAAAGTGGCGCTTGCAGAACTAAG 6117
QY 551 LysAsnGluGluIleLeuCysIleuAlaAsp-----560
      :|:|:|:|:|:|
Db 6118 CAACACACAGCTTGAAACAGCCGGGATTTACTACGTAAAGGCACACGGAATCCGTAT 6177
QY 561 -----AspLeuAlaThrArgLeuThrGlyValTyr 570
      :|:|:|:|:|:|
Db 6178 CTGCGGATTAAAGAAACGCAACCCAAATGAGCTTAAACAGCGCACTGTACAAACCAAA 6237
QY 571 ProAlaThrAspAsnPhe-----AlaAlaAlaValSer 581
      :|:|:|:|:|:|
Db 6238 TCAGCGCAGACAGCTGCTTACAGGACCGCCTTATTTAGGGCGCGCGCTGTCTCT 6297
QY 582 AlaPheAlaAlaAsnMetLeuSerSerValIleuLysSerGlu-----AlaThrSerSer 599
      :|:|:|:|:|:|
Db 6298 ACCTTACCAATTTACATCAACCAACCGATGAAATAATACGGTCCGTACAGAGTGGC 6357
QY 600 IleIleLysSerValGlyIleuThrAla 608
      :|:|:|:|:|:|
Db 6358 ATTAGCTTAAACAGCCAAACACACAGCA 6384

RESULT 2
US-09-070-927A-150
; Sequence 150, Application US/09070927A
; Patent No. US20020120116A1
; GENERAL INFORMATION:
; APPLICANT: Charles A. Kunsch
;           Patrick J. Dillon
;           Steven Barash
; TITLE OF INVENTION: Enterococcus faecialis Polynucleotides and Polypeptides
; NUMBER OF SEQUENCES: 982
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/070,927A
; FILING DATE: 04-May-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/046,655
; FILING DATE: 1997-05-16
; APPLICATION NUMBER: 60/044,031
; FILING DATE: 1997-05-06
; APPLICATION NUMBER: 60/066,009
; FILING DATE: 1997-11-14
; ATTORNEY/AGENT INFORMATION:
; NAME: Kenley K. Hoover
; REGISTRATION NUMBER: 40,302

```

```

; REFERENCE/DOCKET NUMBER: PB369
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 150:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11739 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 150:
US-09-070-927A-150

Alignment Scores:
Pred. No.: 0.0206 Length: 11739
Score: 129.00 Matches: 160
Percent Similarity: 31.86% Conservative: 107
Best Local Similarity: 19.09% Mismatches: 255
Query Match: 3.82% Indels: 317
DB: 10 Gaps: 43

US-09-677-653a-50 (1-647) x US-09-070-927A-150 (1-11739)
QY 8 SerGlnArgProHisAsnArgArgGlyThrArgAsnValArgValSerAlaAsnThrVal 27
      :|:|:|:|:|:|
Db 9107 ACGAATCGTAGTCTTAATAGCGGAGTAAGACACCAATATATGTTAGTAACAATCTTGT 9166
QY 28 ThrValAsnGlyArgArgAsnGlnArg-----36
      :|:|:|:|:|:|
Db 9167 GGAAACAAAGGACAGCTTCATTAAGGAATCTGTCTACTATTAATTAATTAATTTAT 9226
QY 37 -----ArgArgThrGlyArgGlnValSerProProAsp 47
      :|:|:|:|:|:|
Db 9227 TACAAAAGCTTATGAGAAATTTGTTAATAGTACGCAAAATAATACACCACTATCA 9286
QY 48 AsnPheThrAlaAlaIleAsnIleAsnIleAsnIleAsnIleAsnIleAsnIleAsnIle 67
      :|:|:|:|:|:|
Db 9287 GGATTCACACAGGAAGGAAGCGTT-----ATAATAGTGAACGTAACCTTTT 9337
QY 68 ProAlaAsnIleSerSerMetProGlu-----Phe 77
      :|:|:|:|:|:|
Db 9338 AAACAAAGT---GGCACCTTCCAGATACCTATCAAGCAGAGCGCAAAACTATTAAGTTC 9394
QY 78 ArgAsnThrAlaLysGlyLysIle-----85
      :|:|:|:|:|:|
Db 9395 AAAGTTGTGTACAAAGCAAAACCAACCAACACCTTACCAACCAACCAACCAACCAAC 9454
QY 86 -----AspLeu-----87
      :|:|:|:|:|:|
Db 9455 TATCGGTGACTTATTAACAATGATGATTTGACGGTGGTGTATGAGAGATGAGTTT 9514
QY 88 ---AspSerAspSerIleGlyTyrPheLysTyrLeuAspProAlaGlyAlaThrGlu 106
      :|:|:|:|:|:|
Db 9515 TTTGACTTCCAGCGCTGACTATCAATTCGGGTGTGTGAGCAGCTGGAAGAGTA 9574
QY 107 SerAlaArgAlaValGly---GluTyrSerLysIleProAspGlyLeuValLysPheSer 125
      :|:|:|:|:|:|
Db 9575 GATGCTTCAACAAATGGTTGACTTATGACAAATGGCGTGGGAGATGTTTACAAATAT 9634
QY 126 ValAsp-----AlaGlu 129
      :|:|:|:|:|:|
Db 9635 GTCAATGACTGGAAACACTCAGTCTTGAAGAAAGTCAGTTCACCAACCAACCAACAT 9694
QY 130 IleArgGluIleTyr---AsnGluGlyCysProValValThrAspValSerValPro 147
      :|:|:|:|:|:|
Db 9695 TTGAAGAAATGCTTATCTCGCAATCTCTTGAATATCTAGATGATGAGTACAGTAC 9751
QY 148 LeuAspGlyArgGlnThrPheSerLeuSerIlePheSerPhePromet-----162
      :|:|:|:|:|:|
Db 9752 -----CAATATATGTCGGCTAATTTTACCTTTTACCTGCGCAAAATCTATGCGG 9799
QY 163 -----PheArgThrAlaTyrValAlaValAlaAsn 172
      :|:|:|:|:|:|

```

Db 9800 AAAATCAGTGTATTATACAGAGTGTACTTTGATGACGGCTACCTG---TTTCCAAAT 9856  
 Qy 173 ValGluAnLysGluMetSerLeuAspValValAsnAspLeuIleGluThrLeuAsn 192  
 Db 9857 ATCCAAATTAATTAATAGTTGACAGACCAATCTGTTGAAGGCTTACACAA---AAT 9907  
 Qy 193 LeuAlaAspTrp----- 196  
 Db 9908 CTTTCTACTGCTTGAAGCTTAAGAAAGTGGAAACCAATCTGTTGTTTAAACAACCG 9967  
 Qy 197 -----ArgTrpValValAspSer 202  
 Db 9968 ATTCACAGCAGCACAATGATGATGCTGCTTACTTCTGAGAGGATGCTATTAAT 10027  
 Qy 203 GluGluThrPheAsnPheThrAsnAspThrThrTrpValArgIleArgValLeuArg 222  
 Db 10028 CCCGATCTGATA---TCAATACAGCCGCTCTATTATGTA---ATAATATAA 10072  
 Qy 223 ProThrTrpAspValProAspProThrGluGluValArgThrValSerAspTrpArg 242  
 Db 10073 CCTGTCTAC-----TACTAT 10087  
 Qy 243 LeuThrTrpLysAlaIleThr-----CysGluAlaAsnMet 254  
 Db 10088 TTATCCAAACCCGCAAGTGCAGAAACTCTGTAGACACAGCGGTGCCAAATTAACCA 10147  
 Qy 255 ProThrLeuValAspGluGlyPheThrIleGlyGlyGlyGlyGlyGlyGlyGlyGly 274  
 Db 10148 CCACAA-----GCTTACCCAGAGAAACAAACAGCATTTACCGTACCCA 10195  
 Qy 274 rLeuProGluTrpAspValSerGluAlaTrpAlaLeuHisThrLeuThrPheAlaArg 294  
 Db 10196 TACACCTTCA---AACACAGAGGTACTACCTGATACCTACACAAAGCGGTAAAGAC 10252  
 Qy 294 oSerSerAlaAlaAlaLeuAlaPheValIlePheAlaLeuProGluGlyGlyThrAla 314  
 Db 10253 TACAGTTCAAGGCT-----GGTACA--- 10274  
 Qy 314 AlaGlyThrProAlaTrpGlu-----GlnAlaSerSerGlyGlyTyrl 329  
 Db 10275 -AAGGAAACCAAAAC-CGAGCCTTTAACCGACAGCAAGACAGATTTAGG---GT 10329  
 Qy 329 uThrTrpArgHisAsnGly-----ThrThrPhePr 339  
 Db 10330 AACCTATATGATATGATGATTTGATGATGATGATGATGATGATGATGATGAT 10389  
 Qy 339 AlaGlySerValSerTrpValLeuProGluGlyPheAlaLeuGluArgTrpAspProAs 359  
 Db 10390 AGGCTTCTATGCGCAATTTGATGATGATGATGATGATGATGATGATGATGATGAT 10449  
 Qy 359 nasPGLySerTrpThrAspPheAlaSerAlaGlyAspThrValThrPheArg----- 376  
 Db 10450 TTCGAAATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 10509  
 Qy 377 -----GlnValAlaValAspGluValValThrAsnAsnProAlaGlyGly 392  
 Db 10510 CGCCTTTTACCCAATGTAGTAAAGCCGATGACAGCTGACAAATAGTATAG----- 10564  
 Qy 392 yGlySerAlaProThrPheThrValArgValPro-----ProSe 405  
 Db 10565 -----ATTGAACAACAGACTAGCTGATGACCAATTAATTAATTAATTAATTAATTA 10620  
 Qy 405 rAsn-----AlaTrpThrAsnThrValPheArgAsnThrLeu----- 417  
 Db 10621 TGACATTGCTATAGAGGAGTACGCTTAATTAATTAATTAATTAATTAATTAATTA 10680  
 Qy 418 -----LeuGluThrArgProSerSerArgArgLeu----- 427  
 Db 10681 TGTGACAAAGATAGAACTACTGACAGCAGCATGACATGACATGACATGACATGACAT 10740  
 Qy 428 -GluLeuProMetProProAlaAspPheGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 447  
 Db 10741 GGACATTGGGGGCAACCAACCAATGCTTCTCAGACAGCAATTAAT-----CCTATTGA 10794

Qy 447 uGlnSerLeuLeuLysGluThrLeuGlyCysTrpLeuValHisSerLysMetArgAsnPr 467  
 Db 10795 TAAACATTTGTTAAGCAACAGATTAACACTTTCGATAAATTAATTTGGGAAATGG 10854  
 Qy 467 oValPheGln-----LeuThrProAlaSerSerPheGlyAl 479  
 Db 10855 AAGCTTTCCGATATAGTATCCCAAAATGTTATTTAGCAGAAAGTGGCAGTTTCAAG 10914  
 Qy 479 aVal---SerPheAsn---AsnProGlyTrpGluArgThrArgAspLeuProAspTrpTh 497  
 Db 10915 ATTATTCGGGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 10965  
 Qy 497 rGlyIleArgAspSerPheAspGlnAsnMetSerThrAla----- 510  
 Db 10966 AGTCACCGGTAAACAAGTCACCGAAACCTTTGATGATGATGATGATGATGATGATGAT 11025  
 Qy 510 ----- 510  
 Db 11026 ACCAAGAGGCTTCACCAAGCAACAAATACCATGATGACAGACACCTTCAAGTACAC 11085  
 Qy 511 -ValAlaHisPheArgSerLeuSerHisSerCysSerIleValThrLysThrTyrlGly 530  
 Db 11086 AGCCGCAAAAGCCTTGCAGCAACTTAACCGACGTGCAAGACCTTACTTTCCAAAG 11145  
 Qy 530 yTrp---GluGlyValThrAsnValAsnThrProPheGlyGlnPheAlaHisAlaGly 549  
 Db 11146 CTGTGACAAAGCAACAGCAAGCAAGCTTAATCT----- 11176  
 Qy 549 uLeuLysAsnGluGluIleLeuCysLeuAlaAspAspLeuAlaThrArgLeuThrGlyVa 569  
 Db 11177 -----TTAACAAACCCACACCTACCCCAAC 11199  
 Qy 569 lThrProAlaThrAspAsnPheAlaAlaValSerAlaPheAlaAsn---MetLe 588  
 Db 11200 ATATAACAACT-----TTGTAGCGCAATGACGACAT 11232  
 Qy 588 uSerSerValLeuLysSerGlu-----AlaThrSerSerIleIleLysSerValGly 605  
 Db 11233 GACGCGATTTATTAAGAAAGTGCACCAAGCAAGCTGCGTTTAACGCGGACACTACCG 11292  
 Qy 605 yGluThrAla-ValGlyAlaAlaGlnSer---GlyLeuAlaLysLeuPro 620  
 Db 11293 TGAACCGTGACTACGCGCGCAATGTCACCTGCGCGCCACCAATTAACA 11342  
 RESULT 3  
 US-09-821-616-33  
 : Sequence 33, Application US/09821616  
 : Publication No. US20030027290A1  
 : GENERAL INFORMATION:  
 : APPLICANT: Nielsen, Bjarne R.  
 : APPLICANT: Nielsen, Ruby  
 : APPLICANT: Lehmbeck, Jan  
 : TITLE OF INVENTION: Thermostable Glucoamylase  
 : FILE REFERENCE: 5279.200-US  
 : CURRENT FILING DATE: 2001-03-29  
 : PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/199,290  
 : PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-24  
 : PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 1557/97  
 : PRIOR FILING DATE: EARLIER FILING DATE: 1997-12-30  
 : PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 0925/98  
 : PRIOR FILING DATE: EARLIER FILING DATE: 1998-07-10  
 : PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/070,746  
 : PRIOR FILING DATE: EARLIER FILING DATE: 1998-01-08  
 : PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/094,344  
 : PRIOR FILING DATE: EARLIER FILING DATE: 1998-07-28  
 : PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 08/979,673  
 : PRIOR FILING DATE: EARLIER FILING DATE: 1997-11-26  
 : PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/107,657  
 : PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-30  
 : NUMBER OF SEQ ID NOS: 34  
 : SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 33  
; LENGTH: 2748  
; TYPE: DNA  
; ORGANISM: Talaromyces emersonii  
US-09-821-616-33

## Alignment Scores:

Pred. No.:	0.00519	Length:	2748
Score:	125.50	Matches:	103
Percent Similarity:	31.94%	Conservative:	58
Best Local Similarity:	20.44%	Mismatches:	182
Query Match:	3.72%	Indels:	161
DB:	9	Gaps:	23

US-09-677-653a-50 (1-647) x US-09-821-616-33 (1-2748)

```
QY 40 GtYArgGlnValSerProProAspAsn----- 48
DB 1370 GGTAGCGCAATGATATATCCCGACACAGCGTGACTAATTGATTCAGACTCTGGGA 1429
QY 49 -----PheThrAlaAlaAlaGlnAspLeuAlaGlnSerLeuAsp 61
DB 1430 GAAGTAGAAGAGATCTCATTTCTTACAAACCGCGTCGACACACCGCGCC---CTGGTCGAA 1486
QY 62 AlAsnThrValThrPheProAlaAsn-----IleSerSerMetPro 75
DB 1487 GGCATATGACTGGCAGACAGGCTGAAACACACAGCTCTCAACTGCGTCTCTCAGGCCCT 1546
QY 76 GluPhe-----ArgAsnTrp----- 80
DB 1547 CAGTCCCTGTGTTCCTCGACGATCACTGAGCGGATCGATGTCGTGGCAACTTGGT 1606
QY 81 AlAlaGlyIleValSerLeuAspSerIleGlyTrpPheIleValLeuAsp 100
DB 1607 GGCAGCGGTGTTCCCGGACAGAGCGTGAATTCGATTCGGCAGCATCCACACCTTTGAT 1666
QY 101 ProAlaGlyAlaThrGlu-----SerAlaArgAlaValGlyGlu 113
DB 1667 CCGCGCGAGGCTGTGACGACTGACCTTCACGCCGTTCCGCGCCCTGGCTTGGCAAT 1726
QY 114 TyrSerIleProAspGlyLeuValLysPheSerValAspAlaGluIleArgGluIle 133
DB 1727 CACAAGGTGGTCAACGAC-----TCGTCGCGAGATATC 1759
QY 134 TyrAsnGlnIleLysProValValThrAspAlaSerValProLeuAspGlyArg----- 151
DB 1760 TATGCGATCAATCGAGCATCGCAGAGGATCTGCGTGGCAGTGC---GGCCGCTACCT 1816
QY 151 ----- 151
DB 1817 GAGGATGTACACAGGCGGGAACCCCTGTACTGCGCCACAGCAGCGGCTGCCAGAGCAG 1876
QY 152 -----GlnTrp-----SerLeuSerIlePheSer 159
DB 1877 CTTTACGACCCATCTACAGTGGAGAGATGGGCTCGATAGTATACAGGAGCGTTAGT 1936
QY 160 PheProMetThrArgThrAlaIleValAlaValAlaAsnValGluAsnLysGluMetSer 179
DB 1937 CTGCATTTTCCAGGATATCTACCTCTGCGCGC---GTGGGACACCTTAACCTGGC 1993
QY 180 LeuAspValAlaAsnAspLeuIleGluTrpLeuAsnAsnLeuAlaAspTrp----- 196
DB 1994 TCCACGACTTCAACGACATCATCTCGCGCGCTCCACAGCATATGTGTGATATCTAGT 2053
QY 197 -----ArgTyrValValAspSerGlu-----GlnTrp-IleAsnPheThr 209
DB 2054 ATTGCTGCTAGTTTGGCTTACGATTCACAGGTGAAGAAAAAATGAGACTACTAGT 2113
QY 209 AsnAspThrThrTyrTyrValArgIleArgValLeuArgProThrTyrAspValProAs 229
DB 2114 TCTAGGGAATATACCTCTCAGAG-----CGGCTCTTACCGAACAATTC 2161
QY 229 ProThrGluGlyLeuValArgThrValSerAspTyrArgLeuThrTyrLysAla---I 248
```

```
DB 2162 CCGTACAGACGGGACATCCGCTTCTGCTGCTGCGCTGAGCTGTGCTGCTCTCTCC 2221
QY 248 IeThrCysGluAlaAsnMetProThrLeuValAspGlnGlyPheTrpIleGlyGluIle 268
DB 2222 TAAACGCTTCCGCGCGACGAGATCTGCTGCTC----- 2253
QY 268 YrAlaLeuThrProThrSerLeuProGluTrpAspValSerGluAlaTyrAlaLeuHis 288
DB 2254 -----CTGCTTCTGCGCGCGAGAGCTCCGACAGCAGCTCCCTGCTGCT 2302
QY 288 hIeThrThrPheAlaArgProSerSerAlaAlaLeuAlaPheValTrpAlaGlyLeuP 308
DB 2303 CTGCACCTCTGCGACGGGCGCATACAGCAGGCTTACCAACACCGTCTGCGCAAGCTCTG 2362
QY 308 roGlnGly-----GlyThrAlaProAlaGlyThrProAlaTrpGluIle 323
DB 2363 GCTCTGCGACCTCAACACACAGATGAGCGCCCATGACACACTCTACCTCTGTGCTG 2422
QY 323 IAspSerGlyGlyTyrLeuThrTrpArgHisAsnGlyThrThrPheProAlaGlySer 343
DB 2423 TGACCTTCGACGAATCTGACGACAGCTTACGGGGAGACAAATCTGCGCGCTCGA 2482
QY 343 aIserTyrValLeuProGluGlyPheAlaLeuGluArgTyrAspProAsnAspGlySer 363
DB 2483 TC-----CCGAGACTGGGCACT 2500
QY 363 rPThrAspPheAlaSerAlaGlyAspThrValThrPheArgGlnValAlaValAspGlu 383
DB 2501 GG-----TCCACGGCCAGCGCATGCCCTCCGCGCG---GATG 2536
QY 383 aIValValThrAsnAsnProAlaGlyGlyGlySerAlaProThrPheThrValArgVal 403
DB 2537 CTTAACCAACAGCAACCGCTCTG-----TACGTGACCTGAATCTGC 2581
QY 403 roProSerAsnAlaTyrThrAsnThrValPheArgAsn-----ThrLeuLeu 419
DB 2582 CCGCTGCGACAGCTTGTGATACAGTCTTCAAGAAACAGACGAGGAGCAGCATGCTCT 2641
QY 419 IuThrArgProSerSerArgArgLeuGluLeuProMetProProAlaAspPheGlyIle 439
DB 2642 GGAAGAGACCGGACCGGCTGTACACGGTC-----CCAGCTACTGTGGGCGAGA 2692
QY 439 hValAla 441
DB 2693 CTACCGCC 2700

RESULT 4
US-09-815-242-8615
; Sequence 8615, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; TITLE OF INVENTION: Prokaryotes
; FILE REFERENCE: EILITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815, 242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191, 078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206, 848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207, 727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242, 578
; PRIOR FILING DATE: 2000-10-23
```

```

: PRIOR APPLICATION NUMBER: 60/253,625
: PRIOR FILING DATE: 2000-11-27
: PRIOR APPLICATION NUMBER: 60/257,931
: PRIOR FILING DATE: 2000-12-22
: PRIOR APPLICATION NUMBER: 60/269,308
: PRIOR FILING DATE: 2001-02-16
: NUMBER OF SEQ ID NOS: 14110
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 8615
: LENGTH: 7035
: TYPE: DNA
: ORGANISM: Staphylococcus aureus
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (1)...(7035)
: OS-09-815-242-8615

```



QY 364 -----ThAspPheAlaSerAlaGlyAspThrVal 373  
 Db 66139 GAAAAATGCACCTGCAGATCTTCAAGGTCAATGACCTGGCCGAA---GGTGTCCGTAC 66195  
 QY 374 ThPheArgGlnValAlaValAspGlu----- 382  
 Db 66196 TATTTCCGTGTTCTGCAGTAATAATGATAGTGTGGTGAGCCCATGAAATGCCAGAA 66255  
 QY 383 ---ValValValThrasnAsnProAlaGlyGlySerAlaProThrPheThrValArg 401  
 Db 66256 CCAATTGTAGCCACGACAGACGCTGCT----- 66282  
 QY 402 ValProPheSerAsnAlaTyrThrAsnThrValPheArgAsnThrLeuGluThrArg 421  
 Db 66283 ---CCACCTAGG-----AGACTGATGTGTGTAATACAGC 66315  
 QY 422 ProSerSerArgArgLeuGluLeuProMetProProAlaAspPheGlyGlnThrVal--- 440  
 Db 66316 AATTCCTCGCAGCTTGTAGCTTAAACCTGACACAGATGAGGACCCGAGATCACT 66375  
 QY 441 -----AlaAsnAsnPro 444  
 Db 66376 GGCTACCTGCTTGAATGAGACAAAGGATCTGACCTCGGTTGAGCTGTCAACC 66435  
 QY 445 Lys-----IleGluGlnSerLeuLeuGluThrLeuGlyCysTyrLeuVal 460  
 Db 66436 AAACACGTAACCTTTCACAGTAGAGCGCTGTGTGAGAAACGTA-----TATGATTC 66489  
 QY 461 HisSerLysMetArgAsnProValPheGlnLeuThrProAlaSerSerPheGlyAlaVal 480  
 Db 66490 CGTGTGAAGGCCAAGATATGCTGTAGTGAACCCAGACACCTTCTCTCTGTC 66549  
 QY 481 SerPheAsnAsnProGlyTyrGluArgThrArgAspLeuProAspTyrThrGlyIle 499  
 Db 66550 ATCATTAAAGAGCCTCAAAATCGAGCCACCTGCTGACCTC-----ACTGGAAT 66597  
 RESULT 6  
 US-10-025-380-1055  
 ; Sequence 1055, Application US/10025380  
 ; Publication No. US20020182191A1  
 GENERAL INFORMATION:  
 ; APPLICANT: Xu, Jianshun  
 ; APPLICANT: Lodes, Michael J.  
 ; APPLICANT: Secrist, Heather  
 ; APPLICANT: Benson, Darin R.  
 ; APPLICANT: Meagher, Madeleine Joy  
 ; APPLICANT: Stolk, John A.  
 ; APPLICANT: Wang, Tonglong  
 ; APPLICANT: Jiang, Yugu  
 ; APPLICANT: Smith, Carol L.  
 ; APPLICANT: King, Gordon E.  
 ; APPLICANT: Wang, Aijun  
 ; APPLICANT: Clapper, Jonathan D.  
 ; APPLICANT: Skeiky, Gary R.  
 ; APPLICANT: Fanger, Gary R.  
 ; APPLICANT: Veddyck Thomas S.  
 ; APPLICANT: Carter, Darlick  
 TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS  
 FILE REFERENCE: 210121.471C14  
 CURRENT APPLICATION NUMBER: US/10/025.380  
 NUMBER OF SEQ ID NOS: 1129  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 1055  
 ; LENGTH: 2872  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 US-10-025-380-1055  
 Alignment Scores: 0.0415 Length: 2872  
 Pred. No.:

Score: 117.00  
 Percent Similarity: 33.26%  
 Best Local Similarity: 20.87%  
 Query Match: 3.47%  
 DB: 9  
 Matches: 91  
 Conservative: 54  
 Mismatches: 170  
 Indels: 121  
 Gaps: 17  
 US-09-677-653a-50 (1-647) x US-10-025-380-1055 (1-2872)  
 QY 184 AsnAspLeuIleGluThrPheAsnAsnLeuAlaAspThrArg---TyrValValAspSer 202  
 Db 1677 AACACCTCATCTGCCACCTCCACACACCTCAGTGTGGAGATCTACACCTCAGCAT 1736  
 QY 203 GluGlnThrPheAsnPheThrAsnAspThrThrTyrThrValArgIleArgValLeuArg 222  
 Db 1737 CAGTCCAGGCTCACTGAATAATACACGTTACTCG----- 1772  
 QY 223 ProThrThrAspValProAspProThrGluGlyLeuValArgThrValSerAspTyrArg 242  
 Db 1773 ---CAGTACCAACAACACAGGCTCAGTAGGATCTACACCTCTACAGACGCCAG 1829  
 QY 243 LeuThr----- 244  
 Db 1830 ATCACCACCAACAACACTCTCACTGCCAGATGACACAGCTAGGCTGGTGAAGATC 1889  
 QY 245 -----TyrLysAlaIleThrCysGlu-AlaAs 253  
 Db 1890 CACCACCTCCCGTAGCAACACCAAGTCTACTACTCACTCAACAGTGTCACTGCCAGCAC 1949  
 QY 253 nMetProThrLeuValAspGlnGlyPheThrPheGlyGlyGlnThrAlaLeuThrPro-- 272  
 Db 1950 CACGCGAGGCTCAGTAGAGAAATCTACACCGTC-----TACAGCAGCGCCAG 2000  
 QY 273 -----ThrSerLeuProGlnIleThrAspValSerGluAlaIleThrAlaLeuThr 288  
 Db 2001 CTCACCTGAACACACAGTGTCTCCCTGCCAGACCAACCTCACTGTGTTGTAAGCC 2060  
 QY 288 rLeuThrPhe---AlaArgProSerSerAlaAlaAlaLeuAlaPhe-----Va 303  
 Db 2061 TACACCTTCACACAGCGGCGAGCTCACTCACTCAACACAGTGTCACTGAGAGACGAC 2120  
 QY 303 lTrpAlaGlyLeuProGlnGlyGlyThrAlaProAlaGlyThrProAlaTrpGluAla 323  
 Db 2121 CACCTGGGCGCTCAGTAAGAAATCTACAGCTTCCCGGAGCGCCCTCCACCCAAAC 2180  
 QY 323 aserSerGlyGlyTyrLeuThrThrParGlnAsnGly-----ThrPheProAl 340  
 Db 2181 AGGTTACCTGCCACACTCACAACCGCAGACCTCGGTGAGAAATCAACTTCTTCCAG 2240  
 QY 340 aGlySerValSerTyrValLeuProGluGlyPheAlaLeuGluArgTyrAspProAsnAs 360  
 Db 2241 CAGCTCA----- 2247  
 QY 360 pGlySerTrpThrAspPheAlaSerAlaGlyAspThrValThrPheArgGlnValAlaVal 380  
 Db 2248 -----GGCTCACTGTGAACACACACTCACTGCGCCGCTCCACAC 2288  
 QY 380 lAspGluValValThrAsnAsnProAlaGlyGlyGlySerAlaProThrPheThrVal 400  
 Db 2289 CTTGCGCTCTGTGGAGATTCACACCTCAGCCCTCAGTCAAGTCAACGAAACAAAC 2348  
 QY 400 lArgValProPheSerAsnAlaTyrThrAsnThrValPheArgAsnThrLeuGluThr 420  
 Db 2349 AACTTACCCGCGAGTCCACAACACCAAGCTCAGTGAAGAAATCAACACCTTCTACAC 2408  
 QY 420 rArgProSerSerArgArgLeuGluLeuProMetProProAlaAspPheGlyGlnThrVal 440  
 Db 2409 TAGCCCC-----AGATCAACCAAGATGCAACACTCTCCTGCA-----ACCAAC 2453  
 QY 440 lAlaAsnAsnProLysIleGluGlnSerLeuLeuLysGluThrLeuGlyCys----- 457  
 Db 2454 AAGCTCAGCGCTCAGCGAAGAAATCCAGACATCCACAGTCAACAGGCTCAACGACAC 2513  
 QY 458 -----TyrLeuValHl 461



```
Db 2514 AACAGGTTCCCTGACAGCACACCACTCAGGCTTCAGTACAGAACTTAAACTTCCCA 2573
Qy 461 sSerlysmetArqAsnProValPheGlnLeuThrPro-----AlaserSerph 477
Db 2574 CACGACGCAAGGCTCAACAGAGGCAACACCTGCTCCCTGGCAGTACACACAGCTTCATCCCT 2633
Qy 477 eglyAlaValSer-----PheAsnAsnProGlyTyrGlnArgThrArgAspLeuPr 494
Db 2634 TGGTCAACAATCTACAACTCTCCACAGCAGCCGAGGAGACCTGAAACACACTCTTACC 2693
Qy 494 oAspTyrThr-----GlyIleArgasp-----serPheaspGl 505
Db 2694 TGATGACACCATTAACCTCAGGCTCTGGAGGAGCATCTACACCCACCCACAGCAGCACTGG 2753
Qy 505 nasmetSerThrAlaValAlaHisPheArgSerLeuSerHisSerGlySerIleValTh 525
Db 2754 CTCGCTACACACAACACTGACCCCTGCGACCTCCACAAAGCGCTGGCTTCAGGAAGATC 2813
Qy 525 rlySThrTyrGlnGlyTyrPgluGlyValThrAsnValAspThrPro 540.
Db 2814 TACTACTTTCAGAGCTGGCCAAAGCTCAAGTAC--ACAACACT 2856

RESULT 7
US-09-922-217-1055
; Sequence 1055, Application US/09922217
; Patent No. US20020076414A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Lodes, Michael J.
; APPLICANT: Secrist, Heather
; APPLICANT: Benson, Darin R.
; APPLICANT: Meagher, Madeleine Joy
; APPLICANT: Stolk, John A.
; APPLICANT: Wang, Tongtong
; APPLICANT: Jiang, Yugu
; APPLICANT: Smith, Carole Lynn
; APPLICANT: King, Gordon E.
; APPLICANT: Wang, Aijun
; APPLICANT: Clapper, Jonathan D.
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
; TITLE OF INVENTION: OF COLON CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.471C13
; CURRENT APPLICATION NUMBER: US/09/922,217
; CURRENT FILING DATE: 2001-08-03
; NUMBER OF SEQ ID NOS: 1124
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1055
; LENGTH: 2872
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-922-217-1055

Alignment Scores:
Pred. No.: 0.0415 Length: 2872
Score: 117.00 Matches: 91
Percent Similarity: 33.26% Conservative: 54
Best Local Similarity: 20.87% Mismatches: 170
Query Match: 3.47% Indels: 121
DB: 10 Gaps: 17

US-09-677-653a-50 (1-647) x US-09-922-217-1055 (1-2872)

Qy 184 AsnAspLeuIleGluTyrPleuAsnAsnLeuAlaAspTyrArg--TyrValValAspSer 202
Db 1677 AACACCTCATCTGCCCACTCCACAACTCAGCTCGGAGAACTTCAACACTCAGCAT 1736
Qy 203 GlnGlnTyrPleuAsnPheThrAsnAspThrTyrTyrValArgIleArgValLeuArg 222
Db 1737 CAGTCCAGGCTCACTGAATAATACAAAGCTTACCTGG----- 1772
Qy 223 ProThrTyrAspValProAspProThrGlnGlyLeuValArgThrValSerAspTyrArg 242
Db 223 ProThrTyrAspValProAspProThrGlnGlyLeuValArgThrValSerAspTyrArg 242

Db 1773 ---CAGTACCAACAACACAGGCTTCAGTAGGAGATCTACACCTTCTACAGACGCCAG 1829
Qy 243 LeuThr----- 244
Db 1830 ATCACCACCAACAACACTCTACCTGCCAGCAGACAGGCTAGGCTGGTGAAGATC 1889
Qy 245 -----TyrIleAlaIleThrGlyGlu-AlaAs 253
Db 1890 CACCACCTCCCGTAGCCACACAGGTTTACTACTACACAGTGTCACTGCGACAGCAC 1949
Qy 253 nmetProThrLeuValAspGlnGlyPheTyrPleuGlyGlnTyrAlaLeuThrPro-- 272
Db 1950 CAGCGCAGGCTCAGTAGGAATCTACACGCTC-----TACAGCAGACGCCAGG 2000
Qy 273 -----ThrSerLeuProGlnTyrAspValSerGlnAlaTyrAlaLeuHisTh 288
Db 2001 CTCAACTGAACAACACACTGTCTCCCTCCACACACCACTCAGTTGCTGTGAAGGCC 2060
Qy 288 rLeuThrPhe---AlaArgProSerSerAlaAlaLeuAlaPhe-----Va 303
Db 2061 TACACCTTCCACAGCGCGCCAGCTTCACTACACACACACTGTTCCTAGGACAGCAC 2120
Qy 303 lTyrPalaGlyLeuProGlnGlyTyrAlaProAlaGlyTyrProAlaTyrPgluGlnAl 323
Db 2121 CACCTGGCGCTCAGTAGAAGATCTACAGCTTCCCGGAGCGCACCTCCACCCAAAC 2180
Qy 323 aSerSerGlyGlyTyrIleuThrTyrPargHisAnGly-----ThrThrPheProAl 340
Db 2181 AGGGTACCTGCCACACTCCACACCCGACGCTGGGAGGAATCAACTCTCTCCAG 2240
Qy 340 aglySerValSerTyrValLeuProGlnGlyPheAlaLeuGlnArgTyrAspProAsnAs 360
Db 2241 CAGCTCA----- 2247
Qy 360 pGlySerTyrPheAspPheAlaSerAlaGlyAspThrValThrPheArgGlnValAlaVa 380
Db 2248 -----GGCTCACTGMAACAACACTCCTCAGCTCCGCTCCACAC 2288
Qy 380 lAspGlnValValThrAsnAsnProAlaGlyGlyGlySerAlaProThrPheThrVa 400
Db 2289 CTGCGCTGTTGGAGAAATCCACACCTCAGCTCAGTCCAGTCCAAAGCTCAAGAAAC 2348
Qy 400 lArgValProProSerAsnAlaTyrThrAsnThrValPheArgAsnThrLeuGlnTh 420
Db 2349 AACTTACCGGCGAGTCCACACACACAGCTCAGTGAAGAAATCAACACCTTCTACAC 2408
Qy 420 rArgProSerSerArgArgIleuGlnLeuPrometProProAlaAspPheGlyGlnThVa 440
Db 2409 TAGCCCC-----AGATCACCAAGATGCACACTCTCAGCTGCA-----ACCACAAAC 2453
Qy 440 lAlaAsnAsnProLysIleGlnGlnSerLeuLeuGlyGlnThrLeuGlyGlyS----- 457
Db 2454 AAGCTCAGGCTCAGCGAAGATCCAGACATCCACAGTCAACAGGCTCAACGACAC 2513
Qy 458 -----TyrLeuValHj 461
Db 2514 AACAGGTTCCCTGACAGCACACCACTCAGGCTTCAGTACAGAACTTAAACTTCCCA 2573
Qy 461 sSerlysmetArqAsnProValPheGlnLeuThrPro-----AlaserSerph 477
Db 2574 CACGACGCAAGGCTCAACAGAGGCAACACCTGCTCCCTGGCAGTACACACAGCTTCATCCCT 2633
Qy 477 eglyAlaValSer-----PheAsnAsnProGlyTyrGlnArgThrArgAspLeuPr 494
Db 2634 TGGTCAACAATCTACAACTCTCCACAGCAGCCGAGGAGACCTGAAACACACTCTTACC 2693
Qy 494 oAspTyrThr-----GlyIleArgasp-----serPheaspGl 505
Db 2694 TGATGACACCATTAACCTCAGGCTCTGGAGGAGCATCTACACCCACCCACAGCAGCACTGG 2753
Qy 505 nasmetSerThrAlaValAlaHisPheArgSerLeuSerHisSerGlySerIleValTh 525
Db 2754 CTCGCTACACACAACACTGACCCCTGCGACCTCCACAAAGCGCTGGCTTCAGGAAGATC 2813
```

Qy 525 rlysthrTYrGlnGlyTrpGluGlyValThrAsnValAsnThrPro 540  
 : ||||| ||||| : |||||  
 Db 2814 TACTACTTTCAGAGCTGGCCAGCTCAAGTGAC---ACACACACT 2856

## RESULT 8

US-09-833-263-1055  
 ; Sequence 1055, Application US/09833263  
 ; Patent No. US20020110547A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Wang, Aijun  
 ; APPLICANT: Clapper, Jonathan D.  
 ; APPLICANT: Stolk, John A.  
 ; APPLICANT: Meagher, Madeline J.  
 ; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND  
 ; FILE REFERENCE: 210121.471C12  
 ; CURRENT APPLICATION NUMBER: US/09/833,263  
 ; NUMBER OF SEQ ID NOS: 1093  
 ; SOFTWARE: FASTSEQ for Windows Version 3.0  
 ; SEQ ID NO 1055  
 ; LENGTH: 2872  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; US-09-833-263-1055

## Alignment Scores:

Pred. No.:	0.0415	Length:	2872
Score:	117.00	Matches:	91
Percent Similarity:	33.26%	Conservative:	54
Best Local Similarity:	20.87%	Mismatches:	170
Query Match:	3.47%	Indels:	121
DB:	10	Gaps:	17

US-09-677-653a-50 (1-647) x US-09-833-263-1055 (1-2872)

Qy 184 AsnAspLeuIleGluTrpLeuAsnLeuAlaAspTrpArg---TyrValAlaAspSer 202  
 : ||||| ||||| : ||||| ||||| : |||||  
 Db 1677 AACACCTTCATCTGCCACCAACCTCAGTCTGAGATCTCAACCTCAGCAT 1736  
 Qy 203 GluGluTrpIleAsnPheThrAsnAspThrTrpTyrValArgIleArgValLeuArg 222  
 : ||||| ||||| : ||||| ||||| : |||||  
 Db 1737 CAGTCCAGGCTCACTGAAATTAACAGTTACCTGG----- 1772  
 Qy 223 ProThrTyrAspValProAspProThrGluGlyLeuValArgThrValSerAspTyrArg 242  
 : ||||| ||||| : ||||| ||||| : |||||  
 Db 1773 ---CAGTACCAACACACAGGCTCAGTGAAGCATCTACACCTTCTACAGACGCCAG 1829  
 Qy 243 LeuThr----- 244  
 : |||||  
 Db 1830 ATCACCACACACACACTCTCAGTCCAGCATGACAGCCTAGGCGTGGTGAAGATC 1889  
 Qy 245 -----TyrLysAlaIleThrCysGluAlaAs 253  
 : ||||| ||||| : ||||| ||||| : |||||  
 Db 1890 CACCACTCCCTAGCCAAACAGTTTACTACTACACAGTGTACCTGCGACAGCACAC 1949  
 Qy 253 nmetProThrLeuValAspGlnGlyPheTrpIleGlyGlnTyrAlaLeuThrPro-- 272  
 : ||||| ||||| : ||||| ||||| : |||||  
 Db 1950 CACGCGACGCGCTCAGTGAATCAACACGCTC-----TACAGACAGACGCCAG 2000  
 Qy 273 -----ThrSerLeuProGluTyrAspValSerGluAlaTyrAlaLeuHisTh 288  
 : ||||| ||||| : ||||| ||||| : |||||  
 Db 2001 CTCAACTGAAACACAGTTCCTCCGCGACACCAACCTCAGTTCCGTGAAGAGCC 2060  
 Qy 288 rleuThrPhe---AlaArgProSerSerAlaAlaAlaAlaPhe-----Va 303  
 : ||||| ||||| : ||||| ||||| : |||||  
 Db 2061 TACAACCTTTCACACGCGCGCTCACTCACTCAACACACTGTTCACTGAGAGACAC 2120  
 Qy 303 lTrpAlaGlyLeuProGlnGlyGlyThrAlaProAlaGlyThrProAlaTrpGluGlnAl 323  
 : ||||| ||||| : ||||| ||||| : |||||  
 Db 2121 CACCTCGGGCTCACTGAAGATCTACAGCTTCCCGGACGCCAGCTCCACCCAAAC 2180

Qy 323 aSerSerGlyGlyTyrLeuThrTrpAlrGHisAsnGly-----ThrThrPheProAl 340  
 : ||||| ||||| : ||||| ||||| : |||||  
 Db 2181 AGGTTACCTGCCACACTACACCCAGACCTCGGTGAGAAATCAACTCTTCCAG 2240  
 Qy 340 aGlySerValSerTyrValLeuProGluGlyPheAlaLeuGluArgTyrAspProAsn 360  
 : ||||| ||||| : ||||| ||||| : |||||  
 Db 2241 CAGCTCA----- 2247  
 Qy 360 pGlySerTrpThrAspPheAlaSerAlaGlyAspThrValThrPheArgGluValAlaVa 380  
 : ||||| ||||| : ||||| ||||| : |||||  
 Db 2248 -----GGCTCACTGGAACAAACACTCTACCTGCCCGCTCCACAC 2288  
 Qy 380 lAspGluValValThrAsnAsnProAlaGlyGlySerAlaProThrPheThrVa 400  
 : ||||| ||||| : ||||| ||||| : |||||  
 Db 2289 CTCTGGCTCTGTGGAGAAATCCACACCTCAGCCCTCAGTCCAAAGCTCAACGAAACAC 2348  
 Qy 400 lArgValProProSerAsnAlaTyrThrAsnThrValPheArgAsnThrLeuLeuLuh 420  
 : ||||| ||||| : ||||| ||||| : |||||  
 Db 2349 AACTTACCGGCGATCCCAACACCAAGCTCAGTGAAGAAATCAACCTTCTACAC 2408  
 Qy 420 rArgProSerSerArgArgLeuGluLeuProMetProProAlaAspPheGlyGlnThrVa 440  
 : ||||| ||||| : ||||| ||||| : |||||  
 Db 2409 TAGCCCC-----AGATCAACAGATGCAACACTCTACCTGCA-----ACCAACAC 2453  
 Qy 440 lAlaAsnAsnProLysIleGluGlnSerLeuLeuLysGluThrLeuGlyCys----- 457  
 : ||||| ||||| : ||||| ||||| : |||||  
 Db 2454 AAGCTCAGCGTCAGCGAAGAAATCCAGACATCCACAGTCAACAGCTCAACGACACAC 2513  
 Qy 458 -----TyrLeuValHis 461  
 Db 2514 AACAGCGTTCCCTGACAGACACCACTCAGGCTCAGTCAAGAACTTAAACTTCCCA 2573  
 Qy 461 sSerIlyMetArgAsnProValPheGluLeuThrPro-----AlaSerSerPh 477  
 : ||||| ||||| : ||||| ||||| : |||||  
 Db 2574 CAGCAGCCAAAGGCTCAACAGAGCAACACTGTCCCTGGCAGACAGACAGCTTACCT 2633  
 Qy 477 eGlyAlaValSer-----PheAsnAsnProGlyTyrGluArgThrArgAspLeuR 494  
 : ||||| ||||| : ||||| ||||| : |||||  
 Db 2634 TGTTCACACATCTACACCTTCCACAGCGCCAGCGACACTGAAACCACTCTTAC 2693  
 Qy 494 oAspTyrThr-----GlyIleArgAsp-----SerPheAsp 505  
 : ||||| ||||| : ||||| ||||| : |||||  
 Db 2694 TGTATCACCATTAACCTCAGGCTCTGTGAGGATCTTACACCCACACAGACAGCTGG 2753  
 Qy 505 nasMetSerThrAlaValAlaHisPheArgSerLeuSerHisSerCysSerIleValTh 525  
 : ||||| ||||| : ||||| ||||| : |||||  
 Db 2754 CTGCTACACACAAACAGTCAACCCCTGCGAGCTCCACAAAGCGCTGGCTTCAGAGAATC 2813  
 Qy 525 rlysthrTYrGlnGlyTrpGluGlyValThrAsnValAsnThrPro 540  
 : ||||| ||||| : ||||| ||||| : |||||  
 Db 2814 TACTACTTTCAGAGCTGGCCAAAGCTCAAGTGAC---ACACACACT 2856

## RESULT 9

US-09-554-000-1  
 ; Sequence 1, Application US/09554000  
 ; Patent No. US20020165364A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Tsien, Roger Y.  
 ; APPLICANT: Miyawaki, Atsushi  
 ; TITLE OF INVENTION: DETECTION OF ANALYTES  
 ; FILE REFERENCE: 07257/042001  
 ; CURRENT APPLICATION NUMBER: US/09/554,000  
 ; CURRENT FILING DATE: 2000-04-20  
 ; PRIOR APPLICATION NUMBER: 08/818,252  
 ; PRIOR FILING DATE: 1997-03-14  
 ; NUMBER OF SEQ ID NOS: 56  
 ; SOFTWARE: FASTSEQ for Windows Version 4.0  
 ; SEQ ID NO 1  
 ; LENGTH: 1929  
 ; TYPE: DNA  
 ; ORGANISM: Aequorea victoria  
 ; FEATURE:

```

; NAME/KEY: CDS
; LOCATION: (0)...(1926)
US-09-554-000-1

Alignment Scores:
Pred. No.: 0.0255 Length: 1929
Score: 116.50 Matches: 106
Percent Similarity: 36.46% Conservative: 61
Best Local Similarity: 23.14% Mismatches: 154
Query Match: 3.45% Indels: 137
DB: Gaps: 26

US-09-677-653a-50 (1-647) x US-09-554-000-1 (1-1929)

QY 2 GLYAspAlaGlyValAlaSerGlnArgProHis-----AsnArgArgGlyThr 17
   ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 657 GGTCCTCTGAGTTCGTGACCGCCGCCATGACCATGACCACTGACAGAGCA--- 713

QY 18 ArgAsnValArgValSerAlaAsnThrValThrValAsn-----GlyArgArgAsn 34
   ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 714 ---GATTGCAGAGTTCAAAGAGCCTTCATTTTCAGACAGATGGGCGCACCAT 770

QY 35 GlnArgArgArgThr-GlyArgGlnVal-----SerProAspAsn 49
   ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 771 CACCACAAAGAACTTGGCACCCGTTATGAGTCGCTTGACAAACCAACGAA--- 825

QY 49 eThrAlaAlaGlnAspLeuAlaGlnSerLeuAspAlaAsn-----ThrValTh 66
   ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 826 ---GCGAAATTCAGAGATATGATCAATGAAGTCGATGCTGATGCAATGCAATGTA 881

QY 66 rPheProAlaAsnIleSerSerMetProGluPheArgAsnThrAlaLysGlyLysIleAs 86
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 882 CTTTCCGATTTCTTCTACTATGATG-----GCTGAAAAATGAAGA 923

QY 86 pleuAspSer---AspSerIleGlyThrPyrPheLysThrLeuAspProAlaGly---- 103
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 924 CACAGACAGCGAAGAAATCCGAGAAGATCCGTTTTCACAAGATGGGAACGG 983

QY 104 -----AlaThrIleSerAlaAlaArgAlaValGlyGlyLysSerIleProAspG 120
   ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 984 CTACATCAGCGCTGCTAAATTAACGTCACGTCATG-----ACAAACCTCGGGAGAA 1034

QY 120 yLeuValLysPheSerValAspAlaGluIleArgGluIle----- 133
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1035 GTTAAACGATGAGAAGATGATGAAATGATGAAGGAAGCAATATTCATGTCATGCCA 1094

QY 134 -----TyrAsnGluGluCysProValValThrAspValSerValProLeuAspG 151
   ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1095 AGTAACTATGAGAAGTTTGATACAAATGATGACAGCAAGGGG-----GGGAAGAG 1145

QY 151 gGlnTrpSerLeuSerIlePheSerPheProMetPheArgThrAlaTyrValAlaValAl 171
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1146 GCGCTGGAGAAAACCTTCATTGCTC-----GTCACCGCTGC 1181

QY 171 aasn-----ValGluAsnLysGluMetSerLeuAs 181
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1182 CAACCGGTTCAAGAAATCCAGCTCATGCTGAGCAAGGGCGAGCGCTTCCACCGG 1241

QY 181 pValValAsnAspLeuIleGluTrpLeuAsnAsnLeuAlaAspTrpArgTrpValValAs 201
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1242 GGTGTGCTCCATCCTGTGTCAGCGAGGCGGCTAAAGCGGCACAAGTTACACGTGC 1301

QY 201 pSerGluGlnTrpIleAsnPheThrAsnAspThrThrTyr---TyrValArgIleArgVa 220
   ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1302 CCGCGAGGCG-----GAGGGCGATGCCACCTACGCGCAAGCTGACCTCGAAGTT 1349

QY 220 lLeuArgProThrTyrAspValProAspProThrGluGlyLeuValArgThrValSerAs 240
   ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1350 CATTCGACCAACCGGCAAGCTGCCCGCTGCGCCCAACCTCGTGACACAC----- 1401

QY 240 pTyrArgLeuThrTyrLysAlaIleThrCysGluAlaAsnMetProThrLeuValAspG 260
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1402 -----CTGACCTAC-----GGCGTGACGTGCTTACGCCGCTACCGCACCAATGAAG-- 1449

```

```

QY 260 nGlyPheTrpIleGlyGlnTyrAlaLeuThrProThrSerLeuProGlnTyrAspVa 280
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1450 -----CAGCAGACCTTCTTCAAGTCGCGCAATGCCAAGGCTACGT 1490

QY 280 lSerGluAlaTyrAlaLeuHisThrLeuThrPheAlaArg-ProSerSerAlaAlaAl 300
   ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1491 CCAGAGAG-----CGCACCATCTTCTTCAAGAGCA 1520

QY 300 euAlaPheValTrpAlaGlyLeuProGlnGlyThrAlaProAla----- 315
   ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1521 CGGCA-----ACTACAGACCCGCCCGCAGGTGAAGTT 1553

QY 316 -----GlyThrProAlaTrpGluGlnAlaSerSerGlyTyrLeuThrTrpArgHis 334
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1554 CGAGGGCGACACCC---TGGAACCCATCGAGCTTAAGGCGATCGACTTCAAGAGGA 1610

QY 334 snGlyThrThrPheProAlaGlySerValSerTyrValLeuProGluGlyPheAlaLeuG 354
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1611 CGGCAACATCTCTGGGCGACA----- 1630

QY 354 luarGlyraspProAsnAspLysSerTrpThrAspPheAlaSerAlaGlyAspThrVal- 373
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1631 -----AGCTGAGTACAACTACACAGCCACCAACGCTATAT 1667

QY 374 -----ThrPheArgGlnValAlaVal-----AspGluValValThrAsnAsn 389
   ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1668 CATGGCCGACAGCAAGCAAGGCAATCAAGTGAAGTCAAGTCCGCCACACATCGA 1727

QY 389 roAlaGlyGlySerAlaProThrPheThrValArgValProSer 405
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1728 GGAGCGCAGCGTGCAGCTGCCGACACACTACACAGACACCCCATCG 1777

RESULT 10
US-09-554-000-5
; Sequence 5, Application US/09554000
; Patent No. US20020165364A1
; GENERAL INFORMATION:
; APPLICANT: Tsien, Roger Y.
; APPLICANT: Miyawaki, Acsushi
; TITLE OF INVENTION: FLUORESCENT PROTEIN SENSORS FOR
; TITLE OF INVENTION: DETECTION OF ANALYTES
; FILE REFERENCE: 07257/042001
; CURRENT APPLICATION NUMBER: US/09/554,000
; CURRENT FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: 08/818,252
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 1929
; TYPE: DNA
; ORGANISM: Aequorea victoria.
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (0)...(1926)
US-09-554-000-5

Alignment Scores:
Pred. No.: 0.0255 Length: 1929
Score: 116.50 Matches: 105
Percent Similarity: 36.70% Conservative: 62
Best Local Similarity: 23.08% Mismatches: 157
Query Match: 3.45% Indels: 131
DB: Gaps: 25

US-09-677-653a-50 (1-647) x US-09-554-000-5 (1-1929)

QY 2 GLYAspAlaGlyValAlaSerGlnArgProHis-----AsnArgArgGlyThr 17
   ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 657 GGTCCTCTGAGTTCGTGACCGCCGCCATGACCATGACCACTGACAGAGCA--- 713

QY 18 ArgAsnValArgValSerAlaAsnThrValThrValAsn-----GlyArgArgAsn 34

```

```

Db 714 ---GATTGAGAGCTCAAGAACGCTTCATCATATTCGACAGATGGAGCGCACCAT 770
QY 35 GlnArgArgArgThr-GlyArgGlnVal-----SerProProAspAsnPh 49
Db 771 CACCACAAAGGAACCTGGACCCGTTATGAGTCGCTGGACAACCAAGGAA----- 825
QY 49 eThraAlaAlaAlaGlnAspLeuAlaGlnSerLeuAspAlaAsn-----ThraValTh 66
Db 826 ---GCAGAAATTCGACGATATGATCAATGACATGCGTGAATGGCAATGAACATTTA 881
QY 66 rPheProAlaAsnIleSerSerMetProGluPheArgAsnTrpAlaLysGlyLysIleAs 86
Db 882 CTTTCCTGATTTCTTACTATGATG-----GCTAGAAAATATGAAGA 923
QY 86 pleuAspSer---AspSerIleGlyTrpTrpPheLysTrpLeuAspPro-----AlaGly 103
Db 924 CACAGACAGCGAAGGAATTCGACAGACCATTCGTTTGTTCACAGAGATGGAAACGG 983
QY 103 yAlaTrpGlnSerAlaArgAlaValGlyLysTrpSerLysIleProAspGlyLeuValLys 123
Db 984 CTACATCAGCGGTCGTCAGTTACGTACGTCATGACAAACCTGGGGAGAAATTAAACA 1043
QY 123 sPheSerValAspAlaGlnIleArgGlyIle-----Tyr 134
Db 1044 TGAAGAAGTTGATGAATGATTAAGGAGACAGATATCGATGATGCGCCAACTAACTA 1103
QY 134 rAsnGlnGlyLysProValAlaThrAspValSerValProLeuAspGlyLysIleTrpSe 154
Db 1104 TGAAGCTTTGTTCAATGATGACACCAAGGG-----GGAGAGAGGGCGCTGGAA 1154
QY 154 rLeuSerIlePheSerPheProMetPheArgTrpAlaTyrValAlaValAlaAsn---- 172
Db 1155 GAAAACTTCATTGCC-----GTGACGGCGTCCCAACCGGTT 1190
QY 173 -----ValGluAsnLysGluMetSerLeuAspValValAs 184
Db 1191 CAGAAGATCTCCGACCTCATGCTGAGCAAGGCGGAGGCTGTTCAACGGGCTGTGCC 1250
QY 184 nAspLeuIleGlyTrpLeuAsnAsnLeuAlaAspTrpArgTrpValValAspSerGly 204
Db 1251 CATCCGCTGCGAGCTGAGCGGACGCTAAAGCGCCACAAAGTTACGCTGCCGCGAAGG 1310
QY 204 nTrpIleAsnPheThrAsnAspThrTyr---TyrValArgIleArgValLeuArgPr 223
Db 1311 C-----GAGCGGATGCCACCTACCTACGCAAGCTGACCCCTGAAGTTCTGCAC 1358
QY 223 oThrTyrAspValProAspProThrGlnGlyLeuValArgThValSerAspTrpArgLe 243
Db 1359 CACCGGCAAGCTGCGCTGCGCCGACCCCTCGTGCACAC-----CT 1403
QY 243 uThrTrpLysAlaIleThrCysGlnValAsnMetProThrLeuValAspGlnGlyPheTr 263
Db 1404 GACCTAC---GGCGTCGATGCTTCAGCCGCTACCCGACACCATATGAG----- 1449
QY 263 pIleGlyGlyGlnTyrAlaLeuThrProThrSerLeuProGlnTyrAspValSerGlyAl 283
Db 1450 -----CAGACGACGACTTCTCAAGTCGCGCATGCCGAAGGCTACGTCCAGSAG-- 1497
QY 283 eTyrAlaLeuHisThrLeuThrPheAlaArg--ProSerSerAlaAlaAlaLeuAlaPhe 303
Db 1498 -----CGACACCATCTTCTTCMAAGACGACGACGCGCA----- 1525
QY 303 aTrpAlaGlyLeuProGlnGlyGlyThraAlaProAla-----GlyTrp 317
Db 1526 -----ACTACAAAGACCCGCGCGAGGTGAAGTTGAGGGCGA 1562
QY 317 hPheAlaTrpGlnGlnAlaSerSerGlyGlyTyrLeuThrTrpArgHisAsnGlyThr 337
Db 1563 CACCC---TGCTGAACCGCATGAGCTGAAGGCAATGCAAGTTCACAGAGAGCGCAACT 1619
QY 337 hPheProAlaGlySerValSerTyrValLeuProGlnGlyPheAlaLeuGlnArgTyr 357

```

```

Db 1620 CCTGGGCGACA----- 1630
QY 357 sPheAsnAspGlySerTrpThrAspPheAlaSerAlaGlyAspThrVal-----T 374
Db 1631 -----ACGTGAGTACAACTACACAGCCACACAGCTCTATATCTATGCCCCA 1676
QY 374 hPheArgGlnValAlaVal-----AspGluValValTrpAsnAspProAlaGly 392
Db 1677 CAGCAGAGAAGAACGGCATCAAGTGAAGTCAAGATCCGCGACACATGAGAGCGGCA 1736
QY 392 yGlySerAlaProThrPheThrValArgValProSer 405
Db 1737 CGTGACGTCGCGACCTACCAAGCAACACCCCATCG 1777

RESULT 11
US-09-554-000-3
; Sequence 3, Application US/09554000
; Patent No. US20020165364A1
; GENERAL INFORMATION:
; APPLICANT: Tsien, Roger Y.
; APPLICANT: Miyawaki, Atsushi
; TITLE OF INVENTION: DETECTION OF ANALYTES
; FILE REFERENCE: 07257/042001
; CURRENT APPLICATION NUMBER: US/09/554,000
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: 08/818,252
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1959
; TYPE: DNA
; ORGANISM: Aequorea victoria
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (0)...(1956)
US-09-554-000-3

Alignment Scores:
Pred. No.: 0.0261 Length: 1959
Score: 116.50 Matches: 106
Percent Similarity: 36.46% Conservative: 61
Best Local Similarity: 23.14% Mismatches: 154
Query Match: 3.45% Indels: 137
DB: 9 Gaps: 26

US-09-677-653a-50 (1-647) x US-09-554-000-3 (1-1959)
QY 2 GlyAspAlaGlyValAlaSerGlnArgProHis-----AsnArgArgGlyThr 17
Db 657 GGTCCCTGCGAGATGCTGACGCGCCGCGCATGACCAACATGACGAAGAGCA--- 713
QY 18 ArgAsnValArgValSerAlaAsnThrValThrValAsn-----GlyArgArgAsn 34
Db 714 ---GATTGAGAGTTCAAGAACCTTCATATTCGACAAAGATGGAGCGGACCAT 770
QY 35 GlnArgArgArgThr-GlyArgGlnVal-----SerProProAspAsnPh 49
Db 771 CACCACAAAGGAACCTGGACCCGTTATGAGTCGCTGGACAACCAAGGAA----- 825
QY 49 eThraAlaAlaAlaGlnAspLeuAlaGlnSerLeuAspAlaAsn-----ThraValTh 66
Db 826 ---GCAGAAATTCGACGATATGATCAATGACATGCGTGAATGGCAATGAACATTTA 881
QY 66 rPheProAlaAsnIleSerSerMetProGluPheArgAsnTrpAlaLysGlyLysIleAs 86
Db 882 CTTTCCTGATTTCTTACTATGATG-----GCTAGAAAATATGAAGA 923
QY 86 pleuAspSer---AspSerIleGlyTrpTrpPheLysTrpLeuAspProAlaGly----- 103
Db 924 CACAGACAGCGAAGGAATTCGACAGACCATTCGTTTGTTCACAGAGATGGAAACGG 983

```











Db 12001 CAAACCTATGTGGCGCGTGTGGCGGATGGACCTGAGCGTCGCC----- 12048  
QY 271 ThrProThrSerLeuProGlnTyrAspValSerGluAlaThrAlaLeuHisThrLeuThr 290  
Db 12049 -----GTTCCGGCGGTGATGTCAGC---GCCGTGGCTGGCGGATGCGTGACG 12093  
QY 291 PheAlaArgProSerSerAlaAlaAlaLeuAlaPheValThrPalGlyLeuProGlnGly 310  
Db 12094 ATTGCGCGGAGCGGTACACCTCT-----GCCGGAATCCGCTAACG 12135  
QY 311 GlyThrAlaPro-----Ala 315  
Db 12136 GTTACGCGATCCGGTGAAGCGTGCATCTCGCGCGTGGCGGATGACATCAAGCCATTACC 12195  
QY 316 GlyThrProAlaThrProGlnAlaSerSerGlyTyrLeuThrTrpArgHisAsnGly 335  
Db 12196 GCCGATATGATGATCAACGCTGCCGGAAMAAGCGCGGCTTAAAGCTCTCCGACGACCC 12255  
QY 336 ThrThrPheProAlaGlySerValSerTyrValLeuProGlnGlyPheAlaLeuGluArg 355  
Db 12256 TCTGCGCTTGAAGCGGACAACGGTTACCGTCACTTTGGCGGCAAACTTACAGCGCC 12315  
QY 356 TyrAspProAsnAspGlySerTrpThrAspPheAlaSerAlaGlyAspThrValThrPhe 375  
Db 12316 ACGGTGGCTGCGAATGGTCTCTCGAGCAGCACTCGGCTCCGCGGCAATATGGCGCTCTG 12375  
QY 376 Arg-----GlnValAlaValAspGluVal-----Val 384  
Db 12376 CGTATGGCGCATGCCAGCGCACGCGCTCAGCAATGTTAAAGCGCAACAGCGCCACC 12435  
QY 385 ValThrAsnAsnProAlaGlyGlyGlySerAlaProThrPheThrValArgValProPro 404  
Db 12436 ACGACCCACGCTTACAGCGTTGATGCGAGCGCGCAACGGTGACCATTT----- 12483  
QY 405 SerAsnAlaTyrThrAsnThrValPheArgAsnThrLeuLeuGluThrArgProSerSer 424  
Db 12484 -----AATGACATTCGCGCGCATGATGATTTCTTAAAGCGCGCCAGCCGGA 12528  
QY 425 ArgArgLeuGluLeuPro---MetProProAlaAspPheGlyGlnThrValAlaAsnAsn 443  
Db 12529 GCGGCTGTGACCATCACCAGGAGCAGCAGCAGCGGAGCGGAGCGGTG----- 12579  
QY 444 ProLysIleGlnSerLeuLeuLysGluThrLeuGlyCysTyrLeuValHisSerLys 463  
Db 12579 ----- 12579  
QY 464 MetArgAsnProValPheGlnLeuThrProAlaSerSerPheGlyAlaValSerPheAsn 483  
Db 12580 -----ACCGTCACGCTCAAT 12594  
QY 484 AsnProGlyTyrGluArgThr----- 490  
Db 12595 GGCACAAACTACACCGGACCGTACAGAGAGCGAGCGAGCTGACGCTACCGCTCA 12654  
QY 491 ArgAspLeuProAspTyrThrGlyIleArgAspSerPheAspGlnAsnMetSerThrAla 510  
Db 12655 GCCGACTTAACCAACCCGACCGCAGCACTACACCGTGAAACGGCGGTGAGCGACAAA 12714  
QY 511 ValAlaHisPheArgSerLeuSerHisSerCysSerIleValThrLysThrTyrGlnGly 530  
Db 12715 GCCGGAACCCGGCTGGTTAATACAACTGACGGGTGATACGTCCGTT----- 12765  
QY 531 TyrPleuGlyValThrAsnValAsnThrProPheGly-----Gln 543  
Db 12766 -----CCGTCGTACACATCAACAGGTGGAGCGATGATGATCAACGCGAGGAA 12819  
QY 544 PheAlaHisAlaGlyLeuLeuLysAsnGluLutIleLeuCysLeuAlaAspAspLeuAla 563  
Db 12820 CACGCCCAAGGCGAGATCATAGCGGCTCCGCCACTGAGCGGCAACCGGTAGCACCGTG 12879  
QY 564 Thr-----ArgLeuThrGlyValTyrProAlaThrAspAsnPheAla 577  
Db 12880 ACGGTGACTATGCGACAAATACCTTACACAGGTGCTGATGCCAGCGCAACTGAGAGC 12939

QY 578 AlaAlaValSerAlaPheAlaAlaAsnMetLeuSerSerValLeuLysSerGluAlaThr 597  
Db 12940 GTCCGCGTT-----CCGGCAAGCGTGTCTCGGCACTGGCGAATGGCAGGTGACC 12990  
QY 598 ---SerSerIleIleLysSerValGly-GluThrAlaValGlyAlaAlaGlnSerGlyLe 616  
Db 12991 ATCAATGCCAGCGTCACCGATGCCGAGGAAACAGCG----- 13027  
QY 616 ValAlaLysLeuProGlyLeuLeuMetSerValProGly----- 628  
Db 13028 -GCAGCGCTACCCATCAGGTGACGTCATATACCGGCTGCCAGCATTAACCTTAAAGCC 13086  
QY 629 -----LysIleAlaAl 632  
Db 13087 ATCAGCGCGATTAACATCTGTAACGCCCGATGAAAAAGCCAGCGCTTGACCATCAGCGGC 13146  
QY 632 ArgValArgAla---ArgArgAlaArgArgArgAlaAlaArgAla 646  
Db 13147 GGCAGTACGGGGGTGCGGAGCGGCGGCGGAGGTACCGTCAACGCTCA 13192

Search completed: February 27, 2003, 08:39:41  
Job time : 177 secs

